

```

      GCCCCACCACGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAG
1  -----+-----+-----+-----+-----+-----+ 60
      CGGGGTGGTGC GGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTC
      AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys

      GAGGCCGAGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACT
61 -----+-----+-----+-----+-----+-----+ 120
      CTCCGGCTCTTATAGTGCTGCCCCGACGACTTGTGACGTGCAACTTACTCTTATAGTGA
      GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr

      GTCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGATGGAGGTCGGGCAGCAGGCC
121 -----+-----+-----+-----+-----+-----+ 180
      CAGGGTCTGTGGTTTCAATTAAAGATACGGACCTTCTCCTACCTCCAGCCCGTCGTCCGG
      ValProAspThrLysValAsnPheTyrAlaTrpLysArgMetGluValGlyGlnGlnAla

      GTAGAAGTCTGGCAGGGCCTGGCCCTGCTGTGCGAAGCTGTCCTGCGGGGCCAGGCCCTG
181 -----+-----+-----+-----+-----+-----+ 240
      CATCTTCAGACCGTCCCGGACCGGGACGACAGCCTTCGACAGGACGCCCCGGTCCGGGAC
      ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu

      TTGGTCAACTCTTCCCAGCCGTGGGAGCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGT
241 -----+-----+-----+-----+-----+-----+ 300
      AACCAGTTGAGAAGGGTCGGCACCCCTCGGGGACGTCGACGTACACCTATTTTCGGCAGTCA
      LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer

      GGCCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGGGAGCCCAGAAGGAAGCCATCTCC
301 -----+-----+-----+-----+-----+-----+ 360
      CCGGAAGCGTCGGAGTGGTGAGACGAAGCCCAGACCCCTCGGGTCTTCCTTCGGTAGAGG
      GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer

      CCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCCGCAA
361 -----+-----+-----+-----+-----+-----+ 420
      GGAGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGCGTTT
      ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys

      CTCTTCCGAGTCTACTCCAATTTCTCCGGGAAAGCTGAAGCTGTACACAGGGGAGGCC
421 -----+-----+-----+-----+-----+-----+ 480
      GAGAAGGCTCAGATGAGGTTAAAGGAGGCCCTTTTCGACTTCGACATGTGTCCCCTCCGG
      LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla

      TGCAGGACAGGGGACAGATGA (SEQ ID NO:120)
481 -----+-----+ 501
      ACGTCCTGTCCCCTGTCTACT (SEQ ID NO:135)
      CysArgThrGlyAspArg (SEQ ID NO:121)

```

Figure 5